d his

(FILE 'HOME' ENTERED AT 11:52:35 ON 03 MAY 2007)

FILE 'BIOSIS, CAPLUS, EMBASE, MEDLINE, JAPIO' ENTERED AT 11:53:08 ON 03
MAY 2007

```
L1           703 S (ANTIBOD? ARRAY)
L2         35045 S (CELL LYSATE)
L3            27 S L1 AND L2
L4            12 DUPLICATE REMOVE L3 (15 DUPLICATES REMOVED)
L5          9863 S L2 AND ANTIBOD?
L6           615 S L5 AND SCREEN?
L7           227 S L6 AND PD<1998
L8             0 S L7 AND SRRAY?
L9             0 S L7 AND ARRAY?
L10            0 S L7 AND CHIP?
L11         8327 S (BINDING PATTERN)
L12            0 S L11 AND L7
L13           14 S L11 AND L2
L14            5 DUPLICATE REMOVE L13 (9 DUPLICATES REMOVED)
L15          330 S (PROTEIN FINGERPRINTING)
L16            6 S L15 AND L2
L17            2 DUPLICATE REMOVE L16 (4 DUPLICATES REMOVED)
L18           10 S L7 AND PLATE?
L19            5 DUPLICATE REMOVE L18 (5 DUPLICATES REMOVED)
L20           62 S L7 AND ASSAY
L21           31 DUPLICATE REMOVE L20 (31 DUPLICATES REMOVED)
L22           31 S L21 AND PD<1998
L23           29 S L22 NOT L19
L24          990 S (ANTIBOD? PANEL)
L25            0 S L24 AND L2
L26          500 S L24 AND PD<1998
L27            6 S L26 AND L11

=>
```

      DUPLICATE 2
AN   1989:515811 BIOSIS
DN   PREV198988131954; BA88:131954
TI   PROTEIN FINGERPRINTING A NOVEL VIRUS IDENTIFICATION SYSTEM.
AU   WALPITA P [Reprint author]; CONNOR J D; PFEIFER D
CS   DEP PEDIATR, M-009 E, UNIV CALIF, SAN DIEGO, LA JOLLA, CALIF 92093, USA
SO   Journal of Virological Methods, (1989) Vol. 25, No. 3, pp. 315-324.
      CODEN: JVMEDH. ISSN: 0166-0934.
DT   Article
FS   BA
LA   ENGLISH
ED   Entered STN: 15 Nov 1989
      Last Updated on STN: 15 Nov 1989

AB   Viral proteins separated by one-dimensional SDS-PAGE produce protein
      binding patterns (fingerprints) which are unique for
      different viruses. We have applied this concept successfully for the
      development of a practical and objective virus identification system which
      is applicable to most viruses. The method is simple, specific, and,
      unlike the currently available methods, free from all virus-specific
      reagents. Interference by host protein bands in SDS-PAGE preparations of
      virus-infected cell lysates was eliminated
      consistently by treating virus infected cell cultures with optimum
      concentration of NaCl for selective inhibition of host protein synthesis.
      The method utilizes the comparison of protein fingerprints of 'unknown'
      viruses with protein fingerprints of reference viruses stored in a
      computer data base, using pattern recognition software. All 113 'unknown'
      virus strains were correctly identified to the genus level by the protein
      fingerprint method, when compared with the conventional virus
      identification methods.
CC   General biology - Information, documentation, retrieval and computer
      applications   00530
      Cytology - Animal   02506
      Biochemistry methods - Proteins, peptides and amino acids   10054
      Biophysics - Methods and techniques   10504
      Pathology - Diagnostic   12504
      Virology - General and methods   33502
      Virology - Animal host viruses   33506
      Medical and clinical microbiology - General and methods   36001
      Medical and clinical microbiology - Virology   36006
IT   Major Concepts
         Biochemistry and Molecular Biophysics; Computer Applications
         (Computational Biology); Infection; Methods and Techniques;
         Microbiology; Pathology
IT   Miscellaneous Descriptors
         COMPUTER DATA BASE PATTERN RECOGNITION SOFTWARE HOST PROTEIN INHIBITION
         SDS POLYACRYLAMIDE GEL ELECTROPHORESIS
ORGN Classifier
         Viruses   03000
      Super Taxa
         Microorganisms
      Taxa Notes
         Microorganisms, Viruses

AN   1989:515811   BIOSIS
DN   PREV198988131954; BA88:131954
TI   PROTEIN FINGERPRINTING A NOVEL VIRUS IDENTIFICATION SYSTEM.
AU   WALPITA P [Reprint author]; CONNOR J D; PFEIFER D
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       CODEN: JVMEDH. ISSN: 0166-0934.
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       binding patterns (fingerprints) which are unique for
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       is applicable to most viruses. The method is simple, specific, and,
       unlike the currently available methods, free from all virus-specific
       reagents. Interference by host protein bands in SDS-PAGE preparations of
       virus-infected cell lysates was eliminated
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       virus strains were correctly identified to the genus level by the protein
       fingerprint method, when compared with the conventional virus
       identification methods.
CC   General biology - Information, documentation, retrieval and computer
       applications   00530
       Cytology - Animal   02506
       Biochemistry methods - Proteins, peptides and amino acids   10054
       Biophysics - Methods and techniques   10504
       Pathology - Diagnostic   12504
       Virology - General and methods   33502
       Virology - Animal host viruses   33506
       Medical and clinical microbiology - General and methods   36001
       Medical and clinical microbiology - Virology   36006
IT   Major Concepts
          Biochemistry and Molecular Biophysics; Computer Applications
          (Computational Biology); Infection; Methods and Techniques;
          Microbiology; Pathology
IT   Miscellaneous Descriptors
          COMPUTER DATA BASE PATTERN RECOGNITION SOFTWARE HOST PROTEIN INHIBITION
          SDS POLYACRYLAMIDE GEL ELECTROPHORESIS
ORGN   Classifier
          Viruses   03000
       Super Taxa
          Microorganisms
       Taxa Notes
          Microorganisms, Viruses

AN   1985:421101   CAPLUS
DN   103:21101
ED   Entered STN: 27 Jul 1985
TI   Assay for monoclonal antibody against surface Ig of a
       human B cell tumor
IN   Levy, Ronald; Maloney, David G.; Thielemans, Kristiaan
PA   Leland Stanford Junior University, USA
SO   U.S., 10 pp.
       CODEN: USXXAM
DT   Patent
LA   English
IC   ICM G01N033-54
INCL 436518000
CC   15-1 (Immunochemistry)
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI US 4513088	A	19850423	US 1983-480478	19830330 <--
PRAI US 1983-480478		19830330		

CLASS

PATENT NO.	CLASS	PATENT FAMILY CLASSIFICATION CODES
US 4513088	ICM	G01N033-54
	INCL	436518000
	IPCI	G01N0033-54 [ICM,3]
	IPCR	G01N0033-574 [I,C*]; G01N0033-574 [I,A]; G01N0033-68 [I,C*]; G01N0033-68 [I,A]
	NCL	435/007.230; 435/004.000; 435/007.500; 435/007.920; 435/028.000; 435/259.000; 435/948.000; 435/965.000; 435/969.000; 436/518.000; 436/528.000; 436/531.000; 436/548.000; 436/804.000; 436/813.000; 436/823.000

AB   An assay that facilitates screening of hybridoma
       culture media for monoclonal anti-idiotype antibodies,
       particularly murine monoclonal antibodies that are useful for
       treating human B cell tumors is disclosed. The assay is a solid
       phase type assay and involves: incubating a lysate of the
       patient's B cell tumor with immobilized antihuman Ig, separating unbound lysate
       materials, incubating the remaining immobilized complex with the test
       culture medium, separating unbound culture medium material, and incubating the
       remaining immobilized complex with a labeled anti-mouse Ig, separating unbound
       labeled anti-mouse Ig, and detecting the presence of label in the
       remaining immobilized complex. Thus, the sera of 10 patients with B cell
       tumors were analyzed. The idiotypes of 8 patients were IgM, whereas those
       of the other 2 were IgG. In addition, 5 monoclonal anti-idiotypes used in
       the assay reacted only with their corresponding tumor
       cell lysates and not with lysates of other patients.
ST   monoclonal antibody detn B lymphocyte tumor
IT   Enzymes
       RL: BIOL (Biological study)
          (in detection of antibodies to surface Igs of B-cell tumors
          of human)
IT   Neoplasm, composition
          (surface Igs of, antibodies to, detection of, by immunoassay,
          of humans with B-cell tumor)
IT   Immunoglobulins
       RL: PROC (Process)
          (to surface Ig of B cell tumor of human, detection of, by immunoassay)
IT   Lymphocyte
          (B-, surface Igs of tumors of, antibodies to, detection of,
          by immunoassay, of human)
IT   Lymphoma
          (B-cell, surface Igs of human, antibodies to, detection of,
          by immunoassay)

AN   1985:421101   CAPLUS
DN   103:21101
ED   Entered STN: 27 Jul 1985
TI   Assay for monoclonal antibody against surface Ig of a
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US 4513088	ICM	G01N033-54
	INCL	436518000
	IPCI	G01N0033-54 [ICM,3]
	IPCR	G01N0033-574 [I,C*]; G01N0033-574 [I,A]; G01N0033-68 [I,C*]; G01N0033-68 [I,A]
	NCL	435/007.230; 435/004.000; 435/007.500; 435/007.920; 435/028.000; 435/259.000; 435/948.000; 435/965.000; 435/969.000; 436/518.000; 436/528.000; 436/531.000; 436/548.000; 436/804.000; 436/813.000; 436/823.000

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      patient's B cell tumor with immobilized antihuman Ig, separating unbound lysate
      materials, incubating the remaining immobilized complex with the test
      culture medium, separating unbound culture medium material, and incubating the
      remaining immobilized complex with a labeled anti-mouse Ig, separating unbound
      labeled anti-mouse Ig, and detecting the presence of label in the
      remaining immobilized complex. Thus, the sera of 10 patients with B cell
      tumors were analyzed. The idiotypes of 8 patients were IgM, whereas those
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          of humans with B-cell tumor)
IT   Immunoglobulins
      RL: PROC (Process)
          (to surface Ig of B cell tumor of human, detection of, by immunoassay)
IT   Lymphocyte
          (B-, surface Igs of tumors of, antibodies to, detection of,
          by immunoassay, of human)
IT   Lymphoma
          (B-cell, surface Igs of human, antibodies to, detection of,
          by immunoassay)

IT   Immunoglobulins
        RL: PROC (Process)
            (G, to surface Ig of B cell tumor of human, detection of, by
            immunoassay)
IT   Immunoglobulins
        RL: PROC (Process)
            (M, to surface Ig of B cell tumor of human, detection of, by
            immunoassay)
IT   Immunochemical analysis
            (immunoassay, antibodies to surface Igs of B-cell tumors of
            human detection in)

IT   Immunoglobulins
      RL: PROC (Process)
          (G, to surface Ig of B cell tumor of human, detection of, by
          immunoassay)
IT   Immunoglobulins
      RL: PROC (Process)
          (M, to surface Ig of B cell tumor of human, detection of, by
          immunoassay)
IT   Immunochemical analysis
          (immunoassay, antibodies to surface Igs of B-cell tumors of
          human detection in)

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UniProtKB/TrEMBL entry Q4KNZ8

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[Entry history]

[Entry info] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	**Q4KNZ8_9BURK**
Primary accession number	**Q4KNZ8**
Secondary accession numbers	None
Integrated into TrEMBL on	August 2, 2005
Sequence was last modified on	September 5, 2006 (Sequence version 2)
Annotations were last modified on	April 3, 2007 (Entry version 11)

Name and origin of the protein

Protein name	**Hydroxysimazine hydrolase**
Synonyms	None
Gene name	**Name: smzB**
From	Herbaspirillum sp. B601 [TaxID: 321700]
Encoded on	Plasmid pHB1.
Taxonomy	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Oxalobacteraceae; Herbaspirillum.

References

[1] NUCLEOTIDE SEQUENCE.
　　STRAIN=B601;
　　Bazhanov D.P., Zabenkova C.I., Yatsevitch K.K., Bazhanova A.A., Yarmolinsky D.G.;
　　"Simazine-Degrading Herbaspirillum sp. Isolated from Maize Roots in Belarus.";
　　Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.

[2] NUCLEOTIDE SEQUENCE.
　　STRAIN=B601;
　　Yatsevich K.K., Bazhanov D.P., Yarmolinsky D.G.;
　　Submitted (AUG-2006) to the EMBL/GenBank/DDBJ databases.

Comments

Copyright

Cross-references

Sequence databases

EMBL　　　AY965854; AAY40323.2; -; Genomic_DNA.[EMBL / GenBank / DDBJ] [CoDingSequence]

3D structure databases
ModBase   Q4KNZ8.

Organism-specific gene databases
HOGENOM [Family / Alignment / Tree]

Ontologies

GO

GO:0016787; Molecular function: hydrolase activity *(inferred from electronic annotation from UniProtKB-KW)*.
QuickGo
view.

Family and domain databases

InterPro

IPR006680; Amidohydro_1.
IPR011059; Metal-dep_hydro_comp.
Graphical view of domain structure.

Gene3D   G3DSA:1.20.800.10; G3DSA:1.20.800.10; 1.

Pfam

PF01979; Amidohydro_1; 1.
Pfam graphical view of domain structure.

ProDom   [Domain structure / List of seq. sharing at least 1 domain]

Other
UniRef   View cluster of proteins with at least 50% / 90% / 100% identity.

Keywords

Hydrolase; **Plasmid**.

Features
None

Sequence information

Length: **481 AA**   Molecular weight: **52171 Da**   CRC64: **CC3EF0F08E1CDA91** [This is a checksum on the sequence]

```
          10         20         30         40         50         60
  MTTTLYTGFH QLVTGDVAGT VLNGVDILVR DGEIIGLGPD LPRTLAPIGV GQEQGVEVVN

          70         80         90        100        110        120
  CRGLTAYPGL INTHHHFFQA FVRNLAPLDW TQLDVLAWLR KIYPVFALVD EDCIYHSTVV

         130        140        150        160        170        180
  SMAELIKHGC TTAFDHQYNY SRRGGPFLVD RQFDAANLLG LRFHAGRGCI TLPMAEGSTI

         190        200        210        220        230        240
  PDAMRESTDT FLADCERLVS RFHDPRPFAM QRVVVAPCQP VIAYPETFVE SARLARHLGV

         250        260        270        280        290        300
  SLHTHLGEGE TPAMVARFGE RSLDWCENRG FVGPDVWLAH GWEFTAADIA RLAATGTGVA

         310        320        330        340        350        360
  HCPAPVFLVG AEVTDIPAMA AAGVRVGFGV DGHASNDSSN LAECIRLAYL LQCLKASERQ

         370        380        390        400        410        420
  HPVPAPYDFL RMATQGGADC LNRPDLGALA VGRAADFFAV DLNRIEYIGA NHDPRSLPAK

         430        440        450        460        470        480
```

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VGFSGPVDMT VINGKVVWRN GEFPGLDEME LARAADGVFR RVIYGDPLVA ALRRGTGVTP
```

C   Q4KNZ8 in FAST/
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BLAST BLAST submission on ExPASy/SIB or at NCBI (USA)

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

Submit a homology modeling request to SWISS-MODEL

NPSA Sequence analysis tools

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Search [Swiss-Prot/TrEMBL ▾] for [atrazine] [Go] [Clear]

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[Entry history]

UniProtKB/Swiss-Prot entry P72156

[Entry info] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	**ATZA_PSESD**
Primary accession number	**P72156**
Secondary accession numbers	None
Integrated into Swiss-Prot on	July 15, 1998
Sequence was last modified on	May 30, 2000 (Sequence version 2)
Annotations were last modified on	May 1, 2007 (Entry version 43)

Name and origin of the protein

Protein name	**Atrazine chlorohydrolase**
Synonym	**EC 3.8.1.8**
Gene name	**Name: atzA**
From	Pseudomonas sp. (strain ADP) [TaxID: 47660]
Encoded on	Plasmid pADP-1.
Taxonomy	Bacteria; Proteobacteria.

References

[1] NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND PROTEIN SEQUENCE OF 1-10.
   PubMed=8759853 [NCBI, ExPASy, EBI, Israel, Japan]
   de Souza M.L., Sadowsky M.J., Wackett L.P.;
   "Atrazine chlorohydrolase from Pseudomonas sp. strain ADP: gene sequence, enzyme purification, and protein characterization.";
   J. Bacteriol. 178:4894-4900(1996).

[2] SEQUENCE REVISION TO 335 AND 400-406.
   de Souza M.L., Sadowsky M.J., Wackett L.P.;
   Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.

[3] CHARACTERIZATION OF METAL REQUIREMENT.
   DOI=10.1021/bi020415s; PubMed=12450410 [NCBI, ExPASy, EBI, Israel, Japan]
   Seffernick J.L., McTavish H., Osborne J.P., de Souza M.L., Sadowsky M.J., Wackett L.P.;
   "Atrazine chlorohydrolase from Pseudomonas sp. strain ADP is a metalloenzyme.";
   Biochemistry 41:14430-14437(2002).

Comments

- **FUNCTION**: Hydrolytically dechlorinates atrazine to hydroxyatrazine. Dechlorinates also simazine, and desethylatrazine but is not active with melamine, terbutylazine, or desethyldesisopropylatrazine.

- **CATALYTIC ACTIVITY**: Atrazine + H_2O = 4-(ethylamino)-2-hydroxy-6-(isopropylamino)-1,3,5-triazine + HCl.
- **COFACTOR**: Fe(2+).
- **PATHWAY**: Atrazine degradation; first step.
- **SUBUNIT**: Homotetramer.
- **SUBCELLULAR LOCATION**: Cytoplasm *(Potential)*.
- **SIMILARITY**: Belongs to the ATZ/TRZ family.

Copyright

Cross-references

Sequence databases

| EMBL | U55933; AAC64663.1; -; Genomic_DNA.[EMBL / GenBank / DDBJ] [CoDingSequence] |
| PIR | T47197; T47197. |

3D structure databases

ModBase   P72156.

Enzyme and pathway databases

BioCyc   MetaCyc:MONOMER-901; -.

Organism-specific gene databases

HOGENOM [Family / Alignment / Tree]

Ontologies

GO
GO:0018788; Molecular function: atrazine chlorohydrolase activity *(inferred from electronic annotation from EC)*.
QuickGo view.

Family and domain databases

InterPro	IPR006680; Amidohydro_1. IPR011550; Amidohydro_like. IPR011059; Metal-dep_hydro_comp. Graphical view of domain structure.
Gene3D	G3DSA:3.20.20.140; G3DSA:3.20.20.140; 1.
Pfam	PF01979; Amidohydro_1; 1. Pfam graphical view of domain structure.
ProDom	PD001248; Amidohydro_like; 1. [Domain structure / List of seq. sharing at least 1 domain]
BLOCKS	P72156.

Other

| ProtoNet | P72156. |
| UniRef | View cluster of proteins with at least 50% / 90% / 100% identity. |

Keywords

Direct protein sequencing; Hydrolase; Iron; Plasmid.

Features

Feature table viewer

Key	From	To	Length	Description	FTId
CHAIN	1	474	474	Atrazine chlorohydrolase.	PRO_0000122293

Sequence information

Length: **474 AA** [This is the length of the unprocessed precursor]

Molecular weight: **52486 Da** [This is the MW of the unprocessed precursor]

CRC64: **51C1F6C755F141D4** [This is a checksum on the sequence]

```
          10         20         30         40         50         60
  MQTLSIQHGT LVTMDQYRRV LGDSWVHVQD GRIVALGVHA ESVPPPADRV IDARGKVVLP

          70         80         90        100        110        120
  GFINAHTHVN QILLRGGPSH GRQFYDWLFN VVYPGQKAMR PEDVAVAVRL YCAEAVRSGI

         130        140        150        160        170        180
  TTINENADSA IYPGNIEAAM AVYGEVGVRV VYARMFFDRM DGRIQGYVDA LKARSPQVEL

         190        200        210        220        230        240
  CSIMEETAVA KDRITALSDQ YHGTAGGRIS VWPAPATTTA VTVEGMRWAQ AFARDRAVMW

         250        260        270        280        290        300
  TLHMAESDHD ERIHGMSPAE YMECYGLLDE RLQVAHCVYF DRKDVRLLHR HNVKVASQVV

         310        320        330        340        350        360
  SNAYLGSGVA PVPEMVERGM AVGIGTDNGN SNDSVNMIGD MKFMAHIHRA VHRDADVLTP

         370        380        390        400        410        420
  EKILEMATID GARSLGMDHE IGSIETGKRA DLILLDLRHP QTTPHHHLAA TIVFQAYGNE

         430        440        450        460        470
  VDTVLIDGNV VMENRRLSFL PPERELAFLE EAQSRATAIL QRANMVANPA WRSL
```

P72156 in FASTA format

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Report form for errors/updates in this UniProtKB/Swiss-Prot entry

BLAST BLAST submission on ExPASy/SIB or at NCBI (USA)

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

Submit a homology modeling request to SWISS-MODEL

NPSA Sequence analysis tools

Search Swiss-Prot/TrEMBL 🔽 for triazin Go Clear

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Entry history

UniProtKB/TrEMBL entry A0MLT0

[Entry info] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

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Entry information

Entry name	**A0MLT0_9MICC**
Primary accession number	**A0MLT0**
Secondary accession numbers	None
Integrated into TrEMBL on	December 12, 2006
Sequence was last modified on	December 12, 2006 (Sequence version 1)
Annotations were last modified on	February 6, 2007 (Entry version 2)

Name and origin of the protein

Protein name	**Triazine hydrolase**
Synonyms	None
Gene name	None
From	Arthrobacter sp. AD25 [TaxID: 282184]
Taxonomy	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Micrococcineae; Micrococcaceae; Arthrobacter.

References

[1] NUCLEOTIDE SEQUENCE.
   Li Y., Cai B.;
   "The development of a high efficiency atrazine-degrading bacterium by plasmid-assisted molecular breeding.";
   Submitted (SEP-2006) to the EMBL/GenBank/DDBJ databases.

Comments

Copyright

Cross-references

Sequence databases
EMBL   DQ989289; ABK41867.1; -; Genomic_DNA.[EMBL / GenBank / DDBJ] [CoDingSequence]

3D structure databases
ModBase   A0MLT0.

Organism-specific gene databases
HOGENOM [Family / Alignment / Tree]

Ontologies

GO

GO:0016787; Molecular function: hydrolase activity *(inferred from electronic annotation from UniProtKB-KW)*.

QuickGo view.

Family and domain databases

ProDom   [Domain structure / List of seq. sharing at least 1 domain]

Other

UniRef   View cluster of proteins with at least 50% / 90% / 100% identity.

Keywords

Hydrolase.

Features

None

Sequence information

Length: **456 AA**   Molecular weight: **49838 Da**   CRC64: **6113DCAA255C2278** [This is a checksum on the sequence]

```
        10         20         30         40         50         60
MILIRGLTRV ITFDDQEREL EDADILIDGP KIVAVGKDLS DRSVSRTIDG RGMIALPGLI

        70         80         90        100        110        120
NSHQHLYEGA MRAIPQLERV TMASWLEGVL TRSAGWWRDG KFGPDVIREV ARAVLLESLL

       130        140        150        160        170        180
GGITTVADQH LFFPGATADS YIDATIEAAT DLGIRFHAAR SSMTLGKSEG GFCDDLFVEP

       190        200        210        220        230        240
VDRVVQHCLG LIDQYHEPEP FGMVRIALEP CGVPYDKPEL FEAFAQMAAD YDVRLHTHFY

       250        260        270        280        290        300
EPLDAGMSDH LYGMTPWRFL EKHGWASDRV WLAHAVVPPR EEIPEFADAG VAIAHLIAPD

       310        320        330        340        350        360
LRLGWGLAPI REYLDAGITV GFGTTGSASN DGGNLLGDLR LAALAHRPAD PNEPEKWLSA

       370        380        390        400        410        420
RELLRMATRG SAECLGRPDL GVLEEGRAAD IACWRLDGVD RVGVHDPAIG LIMTGLSDRA

       430        440        450
SLVVVNGQVL VENERPVLAD LERIVANTTA LIPKNL
```

A0MLT0 in FAST/ format

View entry in original UniProtKB/TrEMBL format
View entry in raw text format (no links)
Request for annotation of this UniProtKB/TrEMBL entry

BLAST BLAST submission on ExPASy/SIB or at NCBI (USA)

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

Submit a homology modeling request to SWISS-MODEL

NPSA Sequence analysis tools

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